



## 32688sequencelisting.txt

## SEQUENCE LISTING

<110> Geiser, Martin  
Geisse, Sabine  
Ostemeier, Christian  
Ramage, Paul  
Raulf, Friedrich  
Zenke, Gerhard

<120> Three-Dimensional Structure of the  
Catalytic Domain of ZAP-70 Protein Tyrosine Kinase, Methods  
and Use Thereof

<130> 4-32688

<140> US 10/528,709

<141> 2005-03-22

<150> PCT/EP03/10686

<151> 2003-09-25

<150> US 60/413,704

<151> 2002-09-26

<160> 6

<170> FastSEQ for windows Version 4.0

<210> 1

<211> 619

<212> PRT

<213> Homo sapiens

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35 40 45  
Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln  
50 55 60  
Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro  
65 70 75 80  
Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys  
85 90 95  
Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro  
100 105 110  
Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg  
115 120 125  
Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser  
130 135 140  
Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg  
145 150 155 160  
Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys  
165 170 175  
Leu Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg  
180 185 190  
Lys Glu Gln Gly Thr Tyr Ala Leu Ser Leu Ile Tyr Gly Lys Thr Val  
195 200 205  
Tyr His Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro  
210 215 220

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Glu Gly Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys  
 225 230 235 240  
 Leu Lys Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn  
 245 250 255  
 Ser Ser Ala Ser Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala  
 260 265 270  
 His Pro Ser Thr Leu Thr His Pro Gln Arg Arg Ile Asp Thr Leu Asn  
 275 280 285  
 Ser Asp Gly Tyr Thr Pro Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys  
 290 295 300  
 Pro Arg Pro Met Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser  
 305 310 315 320  
 Asp Pro Glu Glu Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn  
 325 330 335  
 Leu Leu Ile Ala Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser Val  
 340 345 350  
 Arg Gln Gly Val Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile  
 355 360 365  
 Lys Val Leu Lys Gln Gly Thr Glu Lys Ala Asp Thr Glu Glu Met Met  
 370 375 380  
 Arg Glu Ala Gln Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg  
 385 390 395 400  
 Leu Ile Gly Val Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu Met  
 405 410 415  
 Ala Gly Gly Pro Leu His Lys Phe Leu Val Gly Lys Arg Glu Glu  
 420 425 430  
 Ile Pro Val Ser Asn Val Ala Glu Leu Leu His Gln Val Ser Met Gly  
 435 440 445  
 Met Lys Tyr Leu Glu Glu Lys Asn Phe Val His Arg Asp Leu Ala Ala  
 450 455 460  
 Arg Asn Val Leu Leu Val Asn Arg His Tyr Ala Lys Ile Ser Asp Phe  
 465 470 475 480  
 Gly Leu Ser Lys Ala Leu Gly Ala Asp Asp Ser Tyr Tyr Thr Ala Arg  
 485 490 495  
 Ser Ala Gly Lys Trp Pro Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn  
 500 505 510  
 Phe Arg Lys Phe Ser Ser Arg Ser Asp Val Trp Ser Tyr Gly Val Thr  
 515 520 525  
 Met Trp Glu Ala Leu Ser Tyr Gly Gln Lys Pro Tyr Lys Lys Met Lys  
 530 535 540  
 Gly Pro Glu Val Met Ala Phe Ile Glu Gln Gly Lys Arg Met Glu Cys  
 545 550 555 560  
 Pro Pro Glu Cys Pro Pro Glu Leu Tyr Ala Leu Met Ser Asp Cys Trp  
 565 570 575  
 Ile Tyr Lys Trp Glu Asp Arg Pro Asp Phe Leu Thr Val Glu Gln Arg  
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Lys	Gln	Ile	Asp	Val	Ala	Ile	Lys	Val	Leu	Lys	Gln	Gly	Thr	Glu	Lys
65	70	75	80												
Ala	Asp	Thr	Glu	Glu	Met	Met	Arg	Glu	Ala	Gln	Ile	Met	His	Gln	Leu
85	90	95													
Asp	Asn	Pro	Tyr	Ile	Val	Arg	Leu	Ile	Gly	Val	Cys	Gln	Ala	Glu	Ala
100	105	110													
Leu	Met	Leu	Val	Met	Glu	Met	Ala	Gly	Gly	Gly	Pro	Leu	His	Lys	Phe
115	120	125													
Leu	Val	Gly	Lys	Arg	Glu	Glu	Ile	Pro	Val	Ser	Asn	Val	Ala	Glu	Leu
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Leu	His	Gln	Val	Ser	Met	Gly	Met	Lys	Tyr	Leu	Glu	Glu	Lys	Asn	Phe
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Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val	Leu	Leu	Val	Asn	Arg	His
165	170	175													
Tyr	Ala	Lys	Ile	Ser	Asp	Phe	Gly	Leu	Ser	Lys	Ala	Leu	Gly	Ala	Asp
180	185	190													
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Lys	Pro	Tyr	Lys	Lys	Met	Lys	Gly	Pro	Glu	Val	Met	Ala	Phe	Ile	Glu
245	250	255													
Gln	Gly	Lys	Arg	Met	Glu	Cys	Pro	Pro	Glu	Cys	Pro	Pro	Glu	Leu	Tyr
260	265	270													
Ala	Leu	Met	Ser	Asp	Cys	Trp	Ile	Tyr	Lys	Trp	Glu	Asp	Arg	Pro	Asp
275	280	285													
Phe	Leu	Thr	Val	Glu	Gln	Arg	Met	Arg	Ala	Cys	Tyr	Tyr	Ser	Leu	Ala
290	295	300													
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Cys	Ala														

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&lt;400&gt; 4

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